

**AMENDMENTS TO THE CLAIMS:**

Claims 1-32, 36-38, 45, 48, 61-63 are canceled without prejudice or disclaimer. Claims 33, 34, 35, 39-44, 46, 47, 58-60 and 64-66 are amended. Claims 49-52 and 54-57 are withdrawn. New claims 67, 68 and 69 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-32. (Canceled.)

33. (Currently amended.) A cutinase variant, wherein the cutinase variant has above ~~80~~90% homology to SEQ ID NO:1 and comprises a ~~modification-substitution~~ of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130, Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the cutinase variant has cutinase activity.

34. (Previously presented.) The cutinase variant claim 33, which comprises the substitution A4V, T29M/I/C, A88H/L/V, N91H, A130V, Q139R, I169A/G/T/V, I178V or R189A/H/V.

35. (Currently amended) The cutinase variant of claim 33, wherein the cutinase variant is a variant of the cutinase from H. ~~umicola~~ insolens strain DSM 1800.

36. (Canceled.)

37. (Canceled.)

38. (Canceled.)

39. (Currently amended.) The cutinase variant of claim 33, wherein the cutinase variant has above 95% homology to SEQ ID NO:1.

40. (Currently amended.) The cutinase variant of claim 33, which cutinase variant further comprises at least one amino acid substitution at a position corresponding to position Q1, L2, E6, G8, E10, S11, A14, N15, A16, F24, V38, N44, L46, E47, S48, H49, R51, D63, L66, S116, S119, G120, L138, T164, T166, L167, I168, L174 and/or ~~E~~179 in SEQ ID NO:1.

41. (Currently amended.) The cutinase variant of claim 33, which cutinase variant further

comprises at least one amino acid substitution at a position corresponding to Q1P/C/L, L2K/Q/V, E6Q, G8D, E10Q, S11C/T, A14P, N15T/D, A16T, F24Y, V38H, N44D, L46I, E47K, S48/E/K, H49Y, R51P, D63N, L66I, S116K, S119P, G120D, L138I, T164S, T166M/I, L167P, I168F, L174F and/or E179Q in SEQ ID NO:1.

42. (Currently amended.) The cutinase variant of claim 33, which cutinase variant further comprises substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.

43. (Currently amended.) The cutinase variant of claim 33, which cutinase variant has hydrolytic activity towards terephthalic acid esters.

44. (Currently amended.) The cutinase variant of claim 33, which cutinase variant has hydrolytic activity towards cyclic tri(ethylene terephthalate) and/or Terephthalic acid bis(2-hydroxyethyl)ester dibenzoate.

45. (Cancelled.)

46. (Currently amended.) The cutinase variant of claim 41, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.

47. (Currently amended.) The cutinase variant of claim 33, wherein the cutinase variant is a variant of a cutinase that has the amino acid sequence of SEQ ID NO:1 and wherein the cutinase variant comprises the substitutions corresponding to E6Q +A14P +E47K +R51P +A130V+E179Q in SEQ ID NO:1.

48. (Cancelled.)

49. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A4.

50. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to T29.

51. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A88.

52. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to N91.

53. (Previously presented.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to A130.

54. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to Q139.

55. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I169.

56. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to I178.

57. (Withdrawn.) The variant of claim 33, wherein the variant comprises a substitution at a position corresponding to R189.

58. (Currently amended.) A cutinase variant, ~~wherein the cutinase variant is a variant of a parent cutinase which is at least 80% homologous to SEQ ID NO:1, wherein the cutinase variant differs from the parent cutinase~~SEQ. ID NO:1 by 1 to 20 substitutions and comprises a ~~modification-substitution~~ of at least one amino acid residue corresponding to position A4, T29, A88, N91, A130 Q139, I169, I178 or R189 in SEQ ID NO:1; and wherein the cutinase variant has cutinase activity.

59. (Currently amended.) A cutinase variant, wherein the cutinase variant has above ~~80~~90% homology to SEQ ID NO:1 and comprises a substitution or substitutions selected from the following group of substitutions in SEQ ID NO:1:

S48E +A88H +N91H +R189V;

Q1L +L2K +G8D +N15D;

N44D +A130V;  
Q1C +L2V +G120D;  
A88L +R189A;  
S48E +L66I +A88L +I169A +R189H;  
A88V +S116K +S119P +Q139R +I169V +R189V;  
A88V +R189A;  
S48K +A88H +I169G +R189H;  
Q1L +L2Q +A4V +S11T;  
T164S;  
L174F;  
H49Y;  
Q1L +L2K +G8D +N15D +S48E +A88H +N91H +R189V;  
Q1L +L2K +G8D +N15D +N44D +A130V;  
Q1L +L2K +G8D +N15D +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +A16T;  
A130V;  
Q1C +L2V;  
G8D +N15D +A16T;  
G8D +N15D +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29M +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29I +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +T29C +S48E +A88H +N91H +A130V +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +L174F +I178V +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +T166M +I168F +R189V;  
G8D +N15D +S48E +A88H +N91H +A130V +T166I +L167P +R189V;  
G8D +N15D +V38H +S48E +A88H +N91H +A130V +I169T +R189V;  
G8D +N15D +V38H +S48E +A88H +N91H +A130V +R189V; and  
G8D +N15D +T29M +S48E +A88H +N91H +A130V +T166I +L167P +R189V;  
and wherein the variant has cutinase activity.

60. (Currently amended.) The cutinase variant of claim 59, wherein the cutinase variant is a variant of the cutinase from Humicola. insolens strain DSM 1800.

61. (Canceled.)

62. (Canceled.)

63. (Canceled.)

64. (Currently amended.) The cutinase variant of claim 59, wherein the cutinase variant has above 95% homology to SEQ ID NO:1.

65. (Currently amended.) The cutinase variant of claim 59, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.

66. (Previously presented.) The cutinase variant of claim 34, further comprising substitutions corresponding to E6Q +A14P +E47K +R51P +E179Q in SEQ ID NO:1.

67. (New.) The cutinase variant of claim 33, wherein the cutinase variant comprises the following substitutions E6Q, G8D, A14P, N15D, E47K, S48E, R51P, A88H, N91H, A130V, E179Q and R189V.

68. (New.) The cutinase variant of claim 35, wherein the cutinase variant comprises the following substitutions E6Q, G8D, A14P, N15D, E47K, S48E, R51P, A88H, N91H, A130V, E179Q and R189V.

69. (New.) The cutinase variant of claim 39, wherein the cutinase variant comprises the following substitutions E6Q, G8D, A14P, N15D, E47K, S48E, R51P, A88H, N91H, A130V, E179Q and R189V.